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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:33:38 ; Search time 21.5 Seconds
(without alignments)

Title: US-10-025-514-8
 Perfect score: 2675
 Sequence: 1 MSQSFKAGVCPPKSAOCL.....IEQNTKSPLFMGKVVNPTOK 503

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 09

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.toxent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.tvirus:*
16: sp.bacteriaph:*
17: sp.archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	2049.5	76.6	418	4	Q96ES1		Q96es1 homo sapien
2	2048.5	76.6	418	4	Q96BF9		Q96bf9 homo sapien
3	1908	71.3	396	6	Q00394		Q00394 cercopithec
4	1484.5	55.5	421	6	Q46319		Q46319 equus caball
5	1480.5	55.3	413	11	O54761		O54761 spermophilu
6	1458.5	54.5	413	11	P97277		P97277 mesocricetu
7	1396	51.8	406	11	G64118		G64118 peromyscus un
8	1352	50.5	413	11	O8VC20		O8vc20 mus musculu
9	1346	50.3	413	11	Q91WH5		Q91wh5 mus musculu
10	1346	50.3	413	11	Q91XB8		Q91xb8 mus musculu
11	1346	50.3	413	11	Q91V74		Q91v74 mus musculu
12	1343.5	50.2	413	6	Q28665		Q28665 oryctolagus
13	1342	50.2	425	11	Q91XC1		Q91xc1 mus musculu
14	1335	49.9	413	11	O8VC41		O8vc41 mus musculu
15	1332	49.8	456	6	O62563		O62663 oryctolagus
16	1326.5	49.6	413	6	Q07298		Q07298 oryctolagus

ALIGNMENTS

RESULT 1

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Q96ESI
ID Q96ESI PRELIMINARY; PRT: 418 AA.
AC Q96ESI;
DT 01-DEC-2001 (TREMBlurel. 19, Created)
DT 01-DEC-2001 (TREMBlurel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlurel. 20, Last annotation update)
DE Similar to serine (or cysteine) proteinase inhibitor, clade A
DE (alpha-1 antiproteinase, antitrypsin), member 1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA STRAUSBERG R.;
RC TISSUE=OVARY;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC EMBL; BC011991; AAH11991.1; -.
CC InterPro; IPR000215; Serpin.
CC Pfam; PF00079; serpin; 1.
CC PROSITE; PS00284; SERPIN; UNKNOWN_1.
CC SERPIN.
WV
WQ SEQUENCE 418 AA; 46722 MW; 70165484573B7F16 CRC64;

Query Match
Best Local Similarity 76.6%; Score 2049.5; DB 4; Length 418;
Matches 398; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

y 96 GMGKSGVSPVKAMEDPGDAAQKTDTSHHDDHPTKNTPNLAEAFSLYRLAQHSN 155
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
14 GLC---CLVPVSLADPGDAAQKTDTSHHDDHPTKNTPNLAEAFSLYRLAQHSN 70

Y 156 STNIFFPVSIATAFAMLSLGTKADTDEILEGNFNLTEIPEAQITHEGFQELLRTLNQ 215
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
b 71 STNIFFPVSIATAFAMLSLGTKADTDEILEGNFNLTEIPEAQITHEGFQELLRTLNQ 130
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

Y 216 DSQQLQITGNGLFTSEGLUKVDKFLVDVKKLYHSEAFITNFGDTEPAKKQINDVYEKGTO 275
|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

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131 DSQQLTTGNGFLSEGLKLVDFLEDKLYHSEAFVNFGEDEAKKQINDIVEKGTQ 190
QY 276 GKIVDLVKELDRDTFALVNYIFFKQWERPEVKDTEEDFHVQDQVTVKVPMMKRLGM 335
Db 191 GKIVDLVKELDRDTFALVNYIFFKQWERPEVKDTEEDFHVQDQVTVKVPMMKRLGM 250
QY 336 FNIHQCKLSSWVLLMKYLGNAITFFLPDEGKLOHLENELTHDITIKFLENERRSASL 395
Db 251 FNIHQCKLSSWVLLMKYLGNAITFFLPDEGKLOHLENELTHDITIKFLENERRSASL 310
QY 396 HLPKLSITGTYDLKSVLGOLGKITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTG 455
Db 311 HLPKLSITGTYDLKSVLGOLGKITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTG 370
QY 456 AAGAMFLEAIPMSIPPEVFNKPFVFLMIEONTKSPFLMGKVVNPOTK 503
Db 371 AAGAMFLEAIPMSIPPEVFNKPFVFLMIDQNTKSPFLMGKVVNPOTK 418

RESULT 2
Q96BF9 PRELIMINARY; PRT; 418 AA.
AC Q96BF9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1
DE antiproteinase, antitrypsin), member 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC015642; AALH5642.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 418 AA; 46708 MW; FF0E525F303542AE CRC64;

Query Match 76.6%; Score 2048.5; DB 4; Length 418;
Best Local Similarity 97.5%; Pred. No. 4.1e-131; Indels 3; Gaps 1;
Matches 398; Conservative 2; Mismatches 5;

QY 96 GWCGRKSCYSPVKAMEDPGDAAQKTDTSHHDDHPTFNKTPNLAEPFSLYRQLAHQSN 155
Db 14 GLC---CLVPVSLAEDPGDAAQKTDTSHHDDHPTFNKTPNLAEPFSLYRQLAHQSN 70
QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILLEGFLNFTLPEAQIHEGFQELLRTLNQ 215
Db 71 STNIFSPVSIATAFAMLSLGTADTHDEILLEGFLNFTLPEAQIHEGFQELLRTLNQ 130
QY 216 DSQQLTTGNGFLSEGLKLVDFLEDKLYHSEAFVNFGEDEAKKQINDIVEKGTQ 275
Db 131 DSQQLTTGNGFLSEGLKLVDFLEDKLYHSEAFVNFGEDEAKKQINDIVEKGTQ 190
QY 276 GKIVDLVKELDRDTFALVNYIFFKQWERPEVKDTEEDFHVQDQVTVKVPMMKRLGM 335
Db 191 GKIVDLVKELDRDTFALVNYIFFKQWERPEVKDTEEDFHVQDQVTVKVPMMKRLGM 250
QY 336 FNIHQCKLSSWVLLMKYLGNAITFFLPDEGKLOHLENELTHDITIKFLENERRSASL 395
Db 251 FNIHQCKLSSWVLLMKYLGNAITFFLPDEGKLOHLENELTHDITIKFLENERRSASL 310
QY 396 HLPKLSITGTYDLKSVLGOLGKITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTG 455
Db 311 HLPKLSITGTYDLKSVLGOLGKITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTG 370

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QY 456 AAGAMFLEAIPMSIPPEVFNKPFVFLMIEONTKSPFLMGKVVNPOTK 503
Db 371 AAGAMFLEAIPMSIPPEVFNKPFVFLMIEONTKSPFLMGKVVNPOTK 418

RESULT 3
O00394 PRELIMINARY; PRT; 396 AA.
AC O00394;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antitrypsin (Fragment).
GN PI.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Sinohara H.;
RT "Cloning and sequencing of complementary DNAs encoding alpha-2-HS
RT glycoprotein, alpha-1-antitrypsin, and beta-actin from african green
RT monkey, Cercopithecus aethiops.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=85026667; PubMed=6333329;
RA Colau B., Chuchana P., Bollen A.;
RT "Revised sequence of full-length complementary DNA coding for human
RT alpha 1-antitrypsin.";
RL DNA 3:327-330(1984).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB004044; BAA20264.1; -.
DR HSSP; P01009; SAPI.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
FT NON_TER
SQ SEQUENCE 396 AA; 44587 MW; 1042EABFAA0A2825 CRC64;

Query Match 71.3%; Score 1908; DB 6; Length 396;
Best Local Similarity 92.9%; Pred. No. 1.3e-121; Indels 0; Gaps 0;
Matches 367; Conservative 19; Mismatches 9;

QY 109 MEDPGDAAQKTDTSHHDDHPTFNKTPNLAEPFSLYRQLAHQSNSTIFFSPVSIAT 168
Db 2 VEDPGDAAQKTDTSHHDDHPTFNKTPNLAEPFSLYRQLAHQSNSTIFFSPVSIAT 61
QY 169 AFAMLSLGTADTHDEILLEGFLNFTLPEAQIHEGFQELLRTLNQDPSQLQTTGNGLF 228
Db 62 AFAMLSLGTADTHDEILLEGFLNFTLPEAQIHEGFQELLRTLNQDPSQLQTTGNGLF 121
QY 229 LSEGLKLVDFLEDKLYHSEAFVNFGEDEAKKQINDIVEKGTQKIVDLVKELDRD 288
Db 122 LNKSVKVVDFLEDKLYHSEAFVNFGEDEAKKQINDIVEKGTQKIVDLVKELDRD 181
QY 289 TVFALVNYIFFKQWERPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNTQHCCKLSSW 348
Db 182 TVFALVNYIFFKQWERPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNTQHCCKLSSW 241
QY 349 LLMKYLGNAITAFFLPDEGKLOHLENELTHDITIKFLENERRSASLHLPKLSITGTYDL 408
Db 242 LLMKYLGNAITAFFLPDEGKLOHLENELTHDITIKFLENERRSASLHLPKLSITGTYDL 301
QY 409 KSVLGOLGKITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMS 468
Db 409 KSVLGOLGKITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLEAIPMS 468

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Db 302 KTVLGLHGIKTVFSGNADLSGVTEADAPLKSKAVHKAVLTIDEKCTEAGAMFLEAIPWS 361
QY 469 IPPEVFNKPPFVLMTEQNTKSPLEMGKVYVNTQK 503
Db 362 IPPEVFNKPPFVLMTEQNTKSPLEMGKVYVNTQK 396

RESULT 4
O46519
ID O46519 PRELIMINARY; PRT; 421 AA.
AC O46519;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antitrypsin.
GN SPI2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ARABIAN BREED;
RA Giffard J.M., Irvin Z.V., Bell T.K., Brandon R.B.;
RT "Equine alpha-1-antitrypsin gene.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AF034077; AAC83412.1;
DR HSSP; P01009; 1KCT.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 421 AA; 46942 MW; D79B101312AC8259 CRC64;

Query Match 55.5%; Score 1484.5; DB 6; Length 421;
Best Local Similarity 68.1%; Pred. No. 8.1e-93;
Matches 282; Conservative 56; Mismatches 73; Indels 3; Gaps 1;

QY 93 CCWGCCKSCVSPVKAMEDPGDAAQKTDTSHHDDQH---PTFNKTTPLNLAFAFSLYRQ 149
Db 8 CLLLLAGLCLVFPSSLAEDLQCAVOETHATAHDEHLQEPAEKHKAPNLDAFASLRH 67
QY 150 LAHQSNSTNFFSPVSIATAFAMLSLGTADTHDELEGNFNLTPEIPAQTHEGFQELL 209
Db 68 VAHQSNSTNFFSPVSIATAFAMLSLGTADTHDELEGNFNLTPEIPAQTHEGFQELL 127
QY 210 RTLNQPSQLTGTGNGLFSEGLKLVDFKLEVDKLYHSEAFVTFNFGDTEAKKQINDY 269
Db 128 NALNHSNQLTGTGNGLFSEGLKLVDFKLEVDKLYHSEAFVTFNFGDTEAKKQINDY 187
QY 270 VEGTGCKIVDLVKELDRDTVFNALVNYIFFKCKWERPEVKDTEEDFHDVQVTVKVP 329
Db 188 VEGTGCKIVDLVKELDRDTVFNALVNYIFFKCKWERPEVKDTEEDFHDVQVTVKVP 247
QY 330 MKRLGMENTHCKLSSWVLLMKYLGITKTVFSGNADLSGVTEAPLKSKAVHKAVLTI 449
Db 248 MHRLLSFDVQYSDTLSSWVLLLDYAGNATAFILLPQGLKQLHLEDTLTKGLAREFLGNR 307
QY 390 RRSASLHLPKLSITGYDLSVGLGKITKTVFSGNADLSGVTEAPLKSKAVHKAVLTI 449
Db 308 SFVNVHLPKLSISGYDLSVGLGKITKTVFSGNADLSGVTEAPLKSKAVHKAVLTI 367
QY 450 DEKGTAAAGFLEAIPMSIPPEVFNKPPFVLMTEQNTKSPLEMGKVYVNTQK 503
Db 368 DEKGTAAAGTTHWEIMPISLPDLKFNRPFLVLIYDRNTKSPLEMGKVYVNTQK 421

RESULT 5
O54761
ID O54761 PRELIMINARY; PRT; 413 AA.
AC O54761;

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DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-antitrypsin-like protein.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tsutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alpha1-antitrypsin-like genes in hibernating
species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB000550; BAA24420.1;
DR HSSP; P01009; 1OLP.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 413 AA; 45953 MW; B08D2544695EE0F4 CRC64;

Query Match 55.3%; Score 1480.5; DB 11; Length 413;
Best Local Similarity 69.6%; Pred. No. 1.5e-92;
Matches 282; Conservative 56; Mismatches 62; Indels 5; Gaps 1;

QY 97 MCGKSCVSPVKAMEDPGDAAQKTDTSHHDDQHPTNKTPLNLAFAFSLYRQLAHQSNS 156
Db 12 LAGLSCLVAGSLAED----AQETGASKHDOEPASHRIAPNLAEFALSILYRLAHESNT 66
QY 157 TNFFSPVSIATAFAMLSLGTADTHDELEGNFNLTPEIPAQTHEGFQELLRLNPD 216
Db 67 TNFFSPVSIATAFAMLSLGTADTHDELEGNFNLTPEIPAQTHEGFQELLRLNPD 126
QY 217 SOLQTTGTGNGLFSEGLKLVDFKLEVDKLYHSEAFVTFNFGDTEAKKQINDYVEKGTQ 276
Db 127 SOLQTTGTGNGLFSEGLKLVDFKLEVDKLYHSEAFVTFNFGDTEAKKQINDYVEKGTQ 186
QY 277 KIVDLVKELDRDTVFNALVNYIFFKCKWERPEVKDTEEDFHDVQVTVKVPMMKRLGMF 336
Db 187 KIVDLVKELDRDTVFNALVNYIFFKCKWERPEVKDTEEDFHDVQVTVKVPMMKRLGMF 246
QY 337 NIQCKKLSWVLLMKYLGITKTVFSGNADLSGVTEAPLKSKAVHKAVLTIIDKGTGA 396
Db 247 EVHYCSTLASWVLLMKYLGITKTVFSGNADLSGVTEAPLKSKAVHKAVLTIIDKGTGA 306
QY 397 LPKLSITGYDLSVGLGKITKTVFSGNADLSGVTEAPLKSKAVHKAVLTIIDKGTGA 456
Db 307 FPKLNTSGTMDLKPVLTRGLITNVSYSKADLSGITDEDDPLRVSQLHKAHLTIDERTGA 366
QY 457 AGAMFLEAIPMSIPPEVFNKPPFVLMTEQNTKSPLEMGKVYVNT 501
Db 367 AGAMFLEAIPMSIPPEVFNKPPFVLMTEQNTKSPLEMGKVYVNT 411

RESULT 6
P97277
ID P97277 PRELIMINARY; PRT; 413 AA.
AC P97277;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Alpha-1-antitrypsinase precursor.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.

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RT and implications for molecular evolution.";

RL J. Biochem. 116:582-588(1994)).

RC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

CC EMBL: S78822; AAB33367.1; -.

DR HSSP: P01009; IOLP.

DR InterPro: IPR000215; Serpin.

DR Pfam: PF000079; serpin; 1.

DR SMART: SM00093; SERPIN; 1.

KW Serpin.

QY SEQUENCE 406 AA; 45126 MW; 814613E44C7AA469 CRC64;

Db

Query Match 51.8%; Score 1386; DB 11; Length 406;

Best Local Similarity 66.6%; Pred. No. 3.7e-86;

Matches 271; Conservative 58; Mismatches 64; Indels 14; Gaps

QY 96 G M C K S C V S P V K A M E D P Q G D A A O K T D T S H D Q D H P T F N K I T N L A E F A F S I Y R O L A H Q S N 155

Db 14 G L C - - - C L V P S F L A E D - - - - - A E K T D S S H - Q D H - - - - - I M A S N L A D F A F G L Y R V L S H Q S N 59

QY 156 S T N I F F S V S T A T A F A M L S L G T K A D T H D E I L G L N F N L T E I P E A Q I H E G F Q E L L T L N Q P 215

Db 60 T T N I F L S P L S T A L A M L S G S K D D T K A Q L L G L H E N L T E T S E A D I H K G F Q H L L K T L N R P 119

QY 216 D S O L Q L T T G N G L F S E G L K I W D F L E D V K K Y L I S E A F T N F G D T E A K K O I N D Y V E K G T O 275

Db 120 N E L Q L I T T G S S I F V N S L N I L V E K E L E E V K N H Y H S E A F F V N F A D S E A K K T I N S F V E K A T H 179

QY 276 G K I V D L V K E L D R D V F A L V N Y I F P K G K W E R P F E V K D T E E D F H V D Q V T V K V P M K R L G M 335

Db 180 G K I V D L V K D L E I D T V A L V N Y I F P R G K W E R F D P E L T E E A D F H V D K S T I V K V P M N R M G M 239

QY 336 F N I O H C K K L S S V I L M K Y L G N A T A I F F L P D E G K L O H L E N E L T H D I I T K F L E N E D R S A S I 395

Db 240 D V H Y C D I L S S V I L L M D Y L G N A T A I F I L P D E G K M Q H L E Q T L T K E H Y K F L O N R H T R S A N V 455

QY 396 H L P K L S I T C Y D L K S V I G O L G I T K V F S N G A D L S G V T E A P L K S K A V H K A V L T I D E K G T E 455

Db 300 H L P K L S I S G T Y N L K K V L S P L G I T Q V F S N G A D L S G I T D V P L K S K A V H K A V L T L D E R G T E 359

QY 456 A A G A M F L E A I P M S I P E V K F N R P F F L M E I Q N T K S P L F M G K V W N P T Q 502

Db 360 A A G T T V L E A V P M S I P D V C F K N P F V V I I C D K H T Q S P L F V G K V W N P T Q 406

RESULT 8

Q8VC20 PRELIMINARY; PRT; 413 AA.

AC Q8VC20; 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)

DE Similar to serine protease inhibitor 1-2 (Hypothetical 45.9 kDa protein).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Strausberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL: BC025109; AAH22109.1; -.

DR EMBL: BC025445; AAH25445.1; -.

DR InterPro: IPR000215; Serpin.

DR Pfam: PF000079; serpin; 1.

DR SMART: SM00093; SERPIN; 1.

DR PROSITE: PS00284; SERPIN; UNKNOWN_1.

NCBI_TaxID=10036;
[1]
RN
RP
SEQUENCE FROM N.A.
RC
TISUE=96004896; PubMed=7548212;
RX
MEDLINE=96004896; PubMed=7548212;
RA
Nakatani T., Suzuki Y., Yoshida K., Sinohara H.;
RT
Molecular cloning and sequence analysis of cDNA encoding plasma
alpha-1-antiproteinase from Syrian hamster: implications for the
RT
evolution of Rodentia.;
RL
Biochim. Biophys. Acta 1263:245-248(1995).
-I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC
EMBL; D49709; BAA08557.1; -.
DR
HSSP; P01009; 9API.
DR
InterPro; IPR000215; Serpin.
DR
Pfam; PF000079; serpin; 1.
DR
SMART; SM00093; SERPIN; 1.
KW
Serpin; Signal.
FT
SIGNAL 1 24 POTENTIAL.
FT
CHAIN 25 413 ALPHA-1-ANTIPROTEINASE.
SQ
SEQUENCE 413 AA; 45819 MW; 71D192E106A1EB36 CRC64;

Query Match 54.5%; Score 1458.5; DB 11; Length 413;
Best Local Similarity 68.6%; Pred. No. 4.6e-91;
Matches 280; Conservative 56; Mismatches 63; Indels 9; Gaps 3;

Qy 96 GCMGKSCVSPVKAMEDPQGDAAOKTDTSHHDQDHTFNKTPNLAFPAFSLYKQLAHQSN 155
Db 14 GLC---CLVPSFLAED----AQETDASKQDQEHQACKIAPNLADFSFLYRELVHQS 65
Qy 156 STNIFFSVSIATAFAMLSIGTKADTHDEILGLNFNLTEIPEAQIHEGFOELLRTLNQ 215
Db 66 TTNIFFSVSIATAFAMLSIGTKGVHTQIQLLEGUGFNLETAEAHVKGPHNLLQTFNRP 125
Qy 216 DSQILQTGTGLFLSEGLKLVDFKDYKLVHSAFTVNFQDTEEAKKQJNDYVVEKGT 275
Db 126 DNEQLQTGTGLFLIHNNKLVDKFLVEEKVNDYSEAFSVNFTDSEAKVINGFVEKGT 185
Qy 276 GKIYDLVKELDRDTVFALVNYIFFKQKWERPEVKDTEEDFHVDDVTVTKVPVPMKRLGM 335
Db 186 GKIYDLVKELDRDQVFLVAVNYIFFKQKWKPPDADNTEADHFVDKTTTKVPVPMKSLGM 245
Qy 336 FNIQCHCKLSWLLMKYLGNAITAEIFFLDPDECKLQHLNELTHDIIITKFLNEDERSASL 395
Db 245 FDIHVSVTLSSWLLMDYLGNAITAEIFFLDPDGKQHLQLETKELIIGFLKDRHTRGANV 305
Qy 396 HLPKLSITGTDLKSVLGQLGITKVFSGNADLSGVTEAPAKLSKXAVHKAVLTIDEGTE 455
Db 306 HFPKLSISGTNYLKTALDPDGLGITQVFSNGADLSGITEVDYPLKGLKXAVHKAVLTIDEGTE 365
Qy 456 AAGAMFLAIPMSIPPEVKFNKPFVFLMIDQNT-KSPLFMGKVNPQTQ 502
Db 366 AAGATFMEIIPMSVPEVNFNSPFIAYIDRQAKSPFLVGKVDPT 413

RESULT 7
Q64118 ID Q64118 PRELIMINARY; PRT; 406 AA.
AC Q64118;
DT 01-NOV-1996 (TREMBLrel. 01. Created)
DT 01-NOV-1996 (TREMBLrel. 01. Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21. Last annotation update)
DE Alpha-1-antiproteinase.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OC NCBI_TaxID=10047;
RN [1]
RP
SEQUENCE FROM N.A.
RX
MEDLINE=95155268; PubMed=7852275;
RA Goto K., Suzuki Y., Yoshida K., Yamamoto K., Sinohara H.;
RT "Plasma alpha-1-antiproteinase from the Mongolian gerbil, Meriones
uniquiculatus: isolation, partial characterization, sequencing of cDNA,
RT

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KW Hypothetical protein; Protease.
SQ SEQUENCE 413 AA; 45896 MW; 12C19B63AAD566E CRC64;

Query Match      50.3%; Score 1352; DB 11; Length 413;
Best Local Similarity 62.6%; Pred. No. 7.8e-84;
Matches 256; Conservative 73; Mismatches 70; Indels 10; Gaps 4;

QY 96 GCMGKSCVSPVKAMEDPOGDAAQKDTSHHQDHPPTFNKIPNLAEAFSLYROLAHOSN 155
DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELHQS 64

QY 156 STNIFSPVSIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHEGFOELLRTLNQ 215
DB 65 TSNIFFSPVSIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHEGFOELLRTLNQ 124

QY 216 DSQQLTTGNGFLSEGLKLVKDFLEDKVKKLYHSEAFVNFQDTEEDFHVDTVTKVPMKRLGM 335
DB 125 DSELQSTGNGFLVNDLKLVEKAEKNHYQAEVSNFAESEAEEAKKVINDEVERGTQ 184

QY 276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPEVKDTEEDFHVDTVTKVPMKRLGM 335
DB 185 GRIVEAVKELDDQDTVFALANVILFKGKWKPFDPENTEEAEFFHVDSTTVKVPMTLSGM 241

QY 336 FNIQCKKLSWVLLMKYLGNAITAFPLPDEGKLOHLENELTHDIITKFLNEEDRRSASL 395
DB 245 LDVHHCSTLSSWVLLMDYAGNATAVFLPDGKMOHLEQTLSEKLSKFLNRRRLAQI 304

QY 396 HLPKLSITGTYDLKSVLGQGLGTTKVFSGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
DB 302 HPRLSISGYNLTKLMSPLGITRIFNNGADLSGITEENAPLKLSKAVHKAVLTIDEKGT 361

QY 455 EAAGAMFLEATPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPQTOK 503
DB 362 EAAAVTVLLAVPYSMPILRFEDHPFLFIIEEHTQSPFLVGKVVDPPTHK 410

RESULT 10
QY1XB8
ID QY1XB8 PRELIMINARY; PRT; 413 AA.
AC QY1XB8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to serine protease inhibitor 1-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC011040; AAH11040.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Protease; Serpin.
KW NON_TER
SQ SEQUENCE 413 AA; 45966 MW; ALFDA1B0C96DFDCC CRC64;

Query Match      50.3%; Score 1346; DB 11; Length 413;
Best Local Similarity 62.3%; Pred. No. 2e-83;
Matches 255; Conservative 72; Mismatches 72; Indels 10; Gaps 4;

QY 96 GCMGKSCVSPVKAMEDPOGDAAQKDTSHHQDHPPTFNKIPNLAEAFSLYROLAHOSN 155
DB 14 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELHQS 64

QY 156 STNIFSPVSIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHEGFOELLRTLNQ 215
DB 65 TSNIFFSPVSIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHEGFOELLRTLNQ 124

QY 216 DSQQLTTGNGFLSEGLKLVKDFLEDKVKKLYHSEAFVNFQDTEEDFHVDTVTKVPMKRLGM 335
DB 125 DSELQSTGNGFLVNDLKLVEKAEKNHYQAEVSNFAESEAEEAKKVINDEVERGTQ 184

QY 276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPEVKDTEEDFHVDTVTKVPMKRLGM 335
DB 185 GRIVEAVKELDDQDTVFALANVILFKGKWKPFDPENTEEAEFFHVDSTTVKVPMTLSGM 244

QY 336 FNIQCKKLSWVLLMKYLGNAITAFPLPDEGKLOHLENELTHDIITKFLNEEDRRSASL 395
DB 245 LDVHHCSTLSSWVLLMDYAGNATAVFLPDGKMOHLEQTLSEKLSKFLNRRRLAQI 304

QY 396 HLPKLSITGTYDLKSVLGQGLGTTKVFSGADLSGVTEE-APLKLSKAVHKAVLTIDEKGT 454
DB 302 HPRLSISGYNLTKLMSPLGITRIFNNGADLSGITEENAPLKLSKAVHKAVLTIDEKGT 361

QY 455 EAAGAMFLEATPMSIPPEVKFNKPFVFLMIEQNTKSPFLMGKVVNPQTOK 503
DB 362 EAAAVTVLLAVPYSMPILRFEDHPFLFIIEEHTQSPFLVGKVVDPPTHK 410

RESULT 9
QY1WH5
ID QY1WH5 PRELIMINARY; PRT; 410 AA.
AC QY1WH5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 45.6 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC015266; AAH15266.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Hypothetical protein; Serpin.
KW NON_TER
SQ SEQUENCE 410 AA; 45622 MW; ED142591DB58F5E2 CRC64;

Query Match      50.3%; Score 1346; DB 11; Length 410;
Best Local Similarity 62.8%; Pred. No. 2e-83;
Matches 257; Conservative 70; Mismatches 72; Indels 10; Gaps 4;

QY 96 GCMGKSCVSPVKAMEDPOGDAAQKDTSHHQDHPPTFNKIPNLAEAFSLYROLAHOSN 155
DB 11 GLC---CLVPSFLAED-----VQETDTSQKQDS-PASHEIATNLGDFALISLYRELHQS 61

QY 156 STNIFSPVSIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHEGFOELLRTLNQ 215
DB 62 TSNIFFSPVSIATAFAMLSLGTAKDTHDEILGLNFIETPEAQIHEGFOELLRTLNQ 121
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[illegible][illegible]

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ID O91XC1 PRELIMINARY; PRT; 425 AA.
AC O91XC1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:4210562) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; BC010988; AAH10988.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
FT NON_TER
SQ SEQUENCE 425 AA; 47157 MW; EA9E50E40C33CAFC CRC64;

Query Match 50.2%; Score 1342; DB 11; Length 425;
Best Local Similarity 62.6%; Pred. No. 3.9e-83;
Matches 256; Conservative 70; Mismatches 73; Indels 10; Gaps 4;

QY 96 GCGKSCVSPVKAMEDPQGDAAQKTDTSHHDDHFTFNKIPNLAFAFSLYROLAHQSN 155
DB 26 GLC---CLVPNLAED-----VOETDTSQKDS-PASHEIATNLGDFALISLYRELVLHQS 76
QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFNLTEIPEAQIHGFEQLLRTLNQ 215
DB 77 TSNIFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQSEADIHKSFOHLQTLNRP 136
QY 216 DSQQLTGTNGGLFSEGLKLVKDFLEVDKLYHSEAFVNFQDTEEAQKQINDYVEKGTQ 275
DB 137 DSELQSLTNGGLFVNDLKLVEKFLBEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQ 196
QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPFVKDTEEDDFHVDQVTVKVPMMKRLGM 335
DB 197 GIAEAVKLDQDTVFALANILFKGKWKQFPDPENTEEAEFHVDESTTVKVPMMTLSGM 256
QY 336 FNIQCHCKLSSVLLMKYLGNAITAFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 395
DB 257 LDVHHCSTLSSVLLMDYAGNATAVFLPDDGKMQLHLEQTLSEKLSKFLNRRRLAQI 316
QY 396 HLPKLSITGYDLKSVLGQGITKVFSGADLSGVTET-APLKLKSAVHKAVLTIDEGKT 454
DB 317 HPRLSISGEYNLKTLSPLGITRIFNNGADLSGITEENAPLKLKSAVHKAVLTIDETGT 376
QY 455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIBQNTKSPFLMGKVVNPQK 503
DB 377 EAAAVTVLLAVPYSMPPILEDHDFLFIIFEEHTQSPFLVGVKVVDPHTK 425

RESULT 14
Q8VC41 PRELIMINARY; PRT; 413 AA.
AC Q8VC41;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to serine protease inhibitor 1-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
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RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021850; AAH21850.1; -.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Protease.
SQ SEQUENCE 413 AA; 45995 MW; C96A4EC0A7951872 CRC64;

Query Match 49.9%; Score 1335; DB 11; Length 413;
Best Local Similarity 62.3%; Pred. No. 1.1e-82;
Matches 255; Conservative 69; Mismatches 75; Indels 10; Gaps 4;

QY 96 GCGKSCVSPVKAMEDPQGDAAQKTDTSHHDDHFTFNKIPNLAFAFSLYROLAHQSN 155
DB 14 GLC---CLVPNLAED-----VOETDTSQKDS-PASHEIATNLGDFALISLYRELVLHQS 64
QY 156 STNIFSPVSIATAFAMLSLGTADTHDEILGLNFNLTEIPEAQIHGFEQLLRTLNQ 215
DB 65 TSNIFSPVSIATAFAMLSLGSKGDTHTQILEGLQFNLTQTAEDIAHKSFQHLQTLNRP 124
QY 216 DSQQLTGTNGGLFSEGLKLVKDFLEVDKLYHSEAFVNFQDTEEAQKQINDYVEKGTQ 275
DB 125 DSELQSLTNGGLFVNDLKLVEKFLBEAKNHYQAEVSVNFAESEAKKVINDFVEKGTQ 184
QY 276 GKIVDLVKELDRDTVFALVNYIFFKQKWERPFVKDTEEDDFHVDQVTVKVPMMKRLGM 335
DB 185 GKIVAEVKELDQDTVFALANILFKGKWKQFPDPENTEEAEFHVDESTTVKVPMMTLSGM 244
QY 336 FNIQCHCKLSSVLLMKYLGNAITAFFLPDEGKLOHLENELTHDIITKFLNEDRRSASL 395
DB 245 LDVHHCSTLSSVLLMDYAGNATAVFLPDDGKMQLHLEQTLSEKLSKFLNRRRLAQI 304
QY 396 HLPKLSITGYDLKSVLGQGITKVFSGADLSGVTET-APLKLKSAVHKAVLTIDEGKT 454
DB 305 HPRLSISGEYNLKTLSPLGITRIFNNGADLSGITEENAPLKLKSAVHKAVLTIDETGT 364
QY 455 EAAGAMFLEAIPMSIPPEVKFNKPFVFLMIBQNTKSPFLMGKVVNPQK 503
DB 365 EAAAVTVLLAVPYSMPPILEDHDFLFIIFEEHTQSPFLVGVKVVDPHTK 413

RESULT 15
O62663 PRELIMINARY; PRT; 456 AA.
AC O62663;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AFS-22.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Saito A.;
RT "Protease inhibitory activity of recombinant alpha-1-antitrypsinases
expressed in Escherichia coli.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR EMBL; AB015164; BAA28760.1; -.
DR HSSP; P01009; BAP1.
DR InterPro; IPR000215; Serpin.
DR Pfam; PF00079; serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Serpin.
SQ SEQUENCE 456 AA; 50542 MW; 88E19DF2767F5C07 CRC64;

Query Match 49.8%; Score 1332; DB 6; Length 456;
Best Local Similarity 58.8%; Pred. No. 2e-82;
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Mon Dec 9 12:51:05 2002

Matches 266; Conservative 65; Mismatches 105; Indels 16; Gaps 4;

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Qy 54 TPNPTRRPGKCPVYGGQCLMLNPNPCE---MDGQCKRDLKCMGMCMGKSCVSPVKAME 110
Db 17 TSPWTSPPWASP-----SLLLPALDTESWTPPVSRRAL---LLLAGLGCLLP----- 63
Qy 111 DPQGAQAQKTDTHSHDQDHPFTFNKITNLAFAFSLYROLAHOSSNSTNIFPSPVSIATAF 170
Db 64 GFLADEAQETAVSSHEQDHPACHRIAPSLAEFALSLYREVAHESNTNIFPSPVSIATAF 123
Qy 171 AMLSIGTKADTHDELLEGNENLFEIPEAQIHEGFQELLRTLNQPDSQLQLOLTGNGLFSL 230
Db 124 AMLSIGAKGDTHTQVLEGLKFNLTETAFAQIHDGFRHLLHTVNRPDSELOLAAGNALVWH 183
Qy 231 EGLKLVDFLEEDVKLYHSEAFNVNFGDTEAKKQIINDYVEKGTQGIQVLDVKELDRTV 290
Db 184 ENLKQHFLEDAKNLYQSEAFVDFRDEQAKTKINSHVEKGTGRKIVLDVQELDARTL 243
Qy 291 FALVNYIEFKGKWERPFVKDTEEDRHVDVTVKVPMMKRLGMFNIQHCKKLSWVLL 350
Db 244 LALVNYVFFKGKWEKPFEPENTKEDFHVDTATTVRVPMMSRLGMYVTLHCSTLASTVWL 303
Qy 351 MKYLGNAIAIFLPDEGKLOHLENELTHDIITKFELENEDRSASLHLPKLSITGTYDLKS 410
Db 304 MDYKGNATALFLLPDEGKLOHLEDLTTELIAKFLAKSSLSRVTVRFPKLSISGTYDLKP 363
Qy 411 VLGQGITKVFNSGADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLEAIPMSIP 470
Db 364 LLGKLGITQVFSNDTDLSGITQEALKVSKALHKAVALTIDENGTEAAGATVEYVLYSMP 423
Qy 471 PEVKFNKPFVFLMIEQNTKSPFLMGKVVNPTQ 502
Db 424 QRVTFDRPFLVVIYSHEVKSPLFVGKVVDPTQ 455
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Job time : 23.5 secs